NCBI

Entrez Protein

PubMed   Nucleotide   Protein   Genome   Structure   PMC   Taxonomy   OMIM   Books

Search Protein ▼ for [   ] Go Clear

Display GenPept ▼ Show 20 ▼ Send to ▼

Range: from begin to end   Features: ☑ CDD + Refresh

☐ **1: NP_416275.** Reports glutamate dehydro...[gi:16129715]

BLink, Conserved
Domains, Links

Comment   Features   Sequence

```
LOCUS       NP_416275               447 aa            linear   BCT 27-JAN-2009
DEFINITION  glutamate dehydrogenase, NADP-specific [Escherichia coli str. K-12
            substr. MG1655].
ACCESSION   NP_416275
VERSION     NP_416275.1  GI:16129715
DBSOURCE    REFSEQ: accession NC_000913.2
KEYWORDS    .
SOURCE      Escherichia coli str. K-12 substr. MG1655
  ORGANISM  Escherichia coli str. K-12 substr. MG1655
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1  (residues 1 to 447)
  AUTHORS   Riley,M., Abe,T., Arnaud,M.B., Berlyn,M.K., Blattner,F.R.,
            Chaudhuri,R.R., Glasner,J.D., Horiuchi,T., Keseler,I.M., Kosuge,T.,
            Mori,H., Perna,N.T., Plunkett,G. III, Rudd,K.E., Serres,M.H.,
            Thomas,G.H., Thomson,N.R., Wishart,D. and Wanner,B.L.
  TITLE     Escherichia coli K-12: a cooperatively developed annotation
            snapshot--2005
  JOURNAL   Nucleic Acids Res. 34 (1), 1-9 (2006)
   PUBMED   16397293
   REMARK   Publication Status: Online-Only
REFERENCE   2  (residues 1 to 447)
  AUTHORS   Blattner,F.R., Plunkett,G., Bloch,C.A., Perna,N.T., Burland,V.,
            Riley,M., Collado-Vides,J., Glasner,J.D., Rode,C.K., Mayhew,G.F.,
            Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A., Rose,D.J.,
            Mau,B. and Shao,Y.
  TITLE     The complete genome sequence of Escherichia coli K-12
  JOURNAL   Science 277 (5331), 1453-1474 (1997)
   PUBMED   9278503
REFERENCE   3  (sites)
  AUTHORS   Kang,W.K., Icho,T., Isono,S., Kitakawa,M. and Isono,K.
  TITLE     Characterization of the gene rimK responsible for the addition of
            glutamic acid residues to the C-terminus of ribosomal protein S6 in
            Escherichia coli K12
  JOURNAL   Mol. Gen. Genet. 217 (2-3), 281-288 (1989)
   PUBMED   2570347
REFERENCE   4  (residues 1 to 447)
  AUTHORS   Arnaud,M., Berlyn,M.K.B., Blattner,F.R., Galperin,M.Y.,
            Glasner,J.D., Horiuchi,T., Kosuge,T., Mori,H., Perna,N.T.,
            Plunkett,G. III, Riley,M., Rudd,K.E., Serres,M.H., Thomas,G.H. and
            Wanner,B.L.
  TITLE     Workshop on Annotation of Escherichia coli K-12
  JOURNAL   Unpublished
   REMARK   Woods Hole, Mass., on 14-18 November 2003 (sequence corrections)
REFERENCE   5  (residues 1 to 447)
  AUTHORS   Glasner,J.D., Perna,N.T., Plunkett,G. III, Anderson,B.D.,
            Bockhorst,J., Hu,J.C., Riley,M., Rudd,K.E. and Serres,M.H.
  TITLE     ASAP: Escherichia coli K-12 strain MG1655 version m56
```

```
 JOURNAL    Unpublished
  REMARK    ASAP download 10 June 2004 (annotation updates)
REFERENCE   6  (residues 1 to 447)
  AUTHORS   Hayashi,K., Morooka,N., Mori,H. and Horiuchi,T.
  TITLE     A more accurate sequence comparison between genomes of Escherichia
            coli K12 W3110 and MG1655 strains
  JOURNAL   Unpublished
  REMARK    GenBank accessions AG613214 to AG613378 (sequence corrections)
REFERENCE   7  (residues 1 to 447)
  AUTHORS   Perna,N.T.
  TITLE     Escherichia coli K-12 MG1655 yqiK-rfaE intergenic region, genomic
            sequence correction
  JOURNAL   Unpublished
  REMARK    GenBank accession AY605712 (sequence corrections)
REFERENCE   8  (residues 1 to 447)
  AUTHORS   Rudd,K.E.
  TITLE     A manual approach to accurate translation start site annotation: an
            E. coli K-12 case study
  JOURNAL   Unpublished
REFERENCE   9  (residues 1 to 447)
  CONSRTM   NCBI Genome Project
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JAN-2009) National Center for Biotechnology
            Information, NIH, Bethesda, MD 20894, USA
REFERENCE   10 (residues 1 to 447)
  AUTHORS   Rudd,K.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-DEC-2008) Department of Biochemistry and Molecular
            Biology, University of Miami Miller School of Medicine, 118 Gautier
            Bldg., Miami, FL 33136, USA
  REMARK    Annotation update from ecogene.org as a multi-database
            collaboration
REFERENCE   11 (residues 1 to 447)
  AUTHORS   Rudd,K.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAR-2008) Department of Biochemistry and Molecular
            Biology, University of Miami Miller School of Medicine, 118 Gautier
            Bldg., Miami, FL 33136, USA
  REMARK    Annotation update from ecogene.org as a multi-database
            collaboration
REFERENCE   12 (residues 1 to 447)
  AUTHORS   Rudd,K.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-SEP-2007) Department of Biochemistry and Molecular
            Biology, University of Miami Miller School of Medicine, 118 Gautier
            Bldg., Miami, FL 33136, USA
  REMARK    Annotation update from ecogene.org as a multi-database
            collaboration
REFERENCE   13 (residues 1 to 447)
  AUTHORS   Rudd,K.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-APR-2007) Department of Biochemistry and Molecular
            Biology, University of Miami Miller School of Medicine, 118 Gautier
            Bldg., Miami, FL 33136, USA
  REMARK    Annotation update from ecogene.org as a multi-database
            collaboration
REFERENCE   14 (residues 1 to 447)
  AUTHORS   Plunkett,G. III.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-FEB-2006) Laboratory of Genetics, University of
            Wisconsin, 425G Henry Mall, Madison, WI 53706-1580, USA
  REMARK    Protein updates by submitter
REFERENCE   15 (residues 1 to 447)
  AUTHORS   Plunkett,G. III.
```

```
     TITLE      Direct Submission
     JOURNAL    Submitted (10-JUN-2004) Laboratory of Genetics, University of
                Wisconsin, 425G Henry Mall, Madison, WI 53706-1580, USA
     REMARK     Sequence update by submitter
  REFERENCE     16 (residues 1 to 447)
     AUTHORS    Plunkett,G. III.
     TITLE      Direct Submission
     JOURNAL    Submitted (13-OCT-1998) Laboratory of Genetics, University of
                Wisconsin, 425G Henry Mall, Madison, WI 53706-1580, USA
  REFERENCE     17 (residues 1 to 447)
     AUTHORS    Blattner,F.R. and Plunkett,G. III.
     TITLE      Direct Submission
     JOURNAL    Submitted (02-SEP-1997) Laboratory of Genetics, University of
                Wisconsin, 425G Henry Mall, Madison, WI 53706-1580, USA
  REFERENCE     18 (residues 1 to 447)
     AUTHORS    Blattner,F.R. and Plunkett,G. III.
     TITLE      Direct Submission
     JOURNAL    Submitted (16-JAN-1997) Laboratory of Genetics, University of
                Wisconsin, 425G Henry Mall, Madison, WI 53706-1580, USA
  COMMENT       PROVISIONAL REFSEQ: This record has not yet been subject to final
                NCBI review. The reference sequence was derived from AAC74831.
                Method: conceptual translation.
  FEATURES             Location/Qualifiers
     source            1..447
                       /organism="Escherichia coli str. K-12 substr. MG1655"
                       /strain="K-12"
                       /sub_strain="MG1655"
                       /db_xref="taxon:511145"
     Protein           1..447
                       /product="glutamate dehydrogenase, NADP-specific"
                       /EC_number="1.4.1.4"
                       /function="enzyme; Amino acid biosynthesis: Glutamate"
                       /calculated_mol_wt=48450
     Region            6..447
                       /region_name="PRK09414"
                       /note="glutamate dehydrogenase; Provisional; PRK09414"
                       /db_xref="CDD:103887"
     Region            57..187
                       /region_name="ELFV_dehydrog_N"
                       /note="Glu/Leu/Phe/Val dehydrogenase, dimerisation domain;
                       pfam02812"
                       /db_xref="CDD:111682"
     Region            202..445
                       /region_name="NADB_Rossmann"
                       /note="Rossmann-fold NAD(P)(+)-binding proteins; cl09931"
                       /db_xref="CDD:127283"
     CDS               1..447
                       /gene="gdhA"
                       /locus_tag="b1761"
                       /gene_synonym="ECK1759"
                       /gene_synonym="JW1750"
                       /coded_by="NC_000913.2:1840395..1841738"
                       /experiment="N-terminus verified by Edman degradation:
                       PMID 6308576,9298646"
                       /GO_component="GO:0005737 - cytoplasm"
                       /GO_process="GO:0006537 - glutamate biosynthetic process"
                       /note="NADP-specific glutamate dehydrogenase"
                       /transl_table=11
                       /db_xref="ASAP:ABE-0005865"
                       /db_xref="UniProtKB/Swiss-Prot:P00370"
                       /db_xref="ECOCYC:EG10372"
                       /db_xref="EcoGene:EG10372"
                       /db_xref="GeneID:946802"
  ORIGIN
```

```
  1 mdqtyslesf lnhvqkrdpn qtefaqavre vmttlwpfle qnpkyrqmsl lerlveperv
 61 iqfrvvwvdd rnqiqvnraw rvqfssaigp ykggmrfhps vnlsilkflg feqtfknalt
121 tlpmgggkgg sdfdpkgkse gevmrfcqal mtelyrhlga dtdvpagdig vggrevgfma
181 gmmkklsnnt acvftgkgls fggslirpea tgyglvyfte amlkrhgmgf egmrvsvsgs
241 gnvaqyaiek amefgarvit asdssgtvvd esgftkekla rlieikasrd grvadyakef
301 glvylegqqp wslpvdialp catqneldvd aahqliangv kavaeganmp ttieatelfq
361 qagvlfapgk aanaggvats glemaqnaar lgwkaekvda rlhhimldih hacvehggeg
421 eqtnyvqgan iagfvkvada mlaqgvi
```
//

NCBI

| PubMed | Nucleotide | Protein | Genome | Structure | PMC | Taxonomy | OMIM | Books |

Protein

Search [Protein ▼] for [   ] [Go] [Clear]

Display [GenPept ▼] Show [20 ▼] [Send to ▼]

Range: from [begin   ] to [end   ]   Features: ☑ CDD [+] [Refresh]

BLink, Conserved
Domains, Links

☐ **1: AAA23868**. Reports glutamate dehydro...[gi:146126]

Comment   Features   Sequence

```
LOCUS       AAA23868                447 aa            linear   BCT 26-APR-1993
DEFINITION  glutamate dehydrogenase.
ACCESSION   AAA23868
VERSION     AAA23868.1  GI:146126
DBSOURCE    locus ECOGDHAK accession K02499.1
KEYWORDS    .
SOURCE      Escherichia coli
  ORGANISM  Escherichia coli
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1  (residues 1 to 447)
  AUTHORS   Valle,F., Becerril,B., Chen,E., Seeburg,P., Heyneker,H. and
            Bolivar,F.
  TITLE     Complete nucleotide sequence of the glutamate dehydrogenase gene
            from Escherichia coli K-12
  JOURNAL   Gene 27 (2), 193-199 (1984)
   PUBMED   6373501
COMMENT     [1] notes a potential ribosome binding site at 178-182.
            Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..447
                     /organism="Escherichia coli"
                     /db_xref="taxon:562"
     Protein         1..447
                     /name="glutamate dehydrogenase"
     Region          6..447
                     /region_name="PRK09414"
                     /note="glutamate dehydrogenase; Provisional; PRK09414"
                     /db_xref="CDD:103887"
     Region          57..187
                     /region_name="ELFV_dehydrog_N"
                     /note="Glu/Leu/Phe/Val dehydrogenase, dimerisation domain;
                     pfam02812"
                     /db_xref="CDD:111682"
     Region          202..445
                     /region_name="NADB_Rossmann"
                     /note="Rossmann-fold NAD(P)(+)-binding proteins; cl09931"
                     /db_xref="CDD:127283"
     CDS             1..447
                     /gene="gdhA"
                     /coded_by="K02499.1:194..1537"
                     /transl_table=11
ORIGIN
        1 mdqtyslesf lnhvqkrdpn qtefaqavre vmttlwpfle qnpkyrqmsl lerlveperv
       61 iqfrvvwvdd rnqiqvnraw rvqfssaigp ykggmrfhps vnlsilkflg feqtfknalt
      121 tlpmgggkgg sdfdpkgkse gevmrfcqal mtelyrhlga dtdvpagdig vggrevgfma
      181 gmmkklsnnt acvftgkgls fggslirpea tgyglvyfte amlkrhgmgf egmrvsvsgs
      241 gnvaqyaiek amefgarvit asdssgtvvd esgftkekla rlieikasrd grvadyakef
```

```
301 glvylegqqp wslpvdialp catqneldvd aahqliangv kavaeganmp ttieatelfq
361 qagvlfapgk aanaggvats glempqnaar lgwkaekvda rlhhimldih hacvehggeg
421 eqtnyvqgan iagfvkvada mlaqgvi
```

//

Last update: Mon, 12 Jan 2009 Rev. 149544

NCBI

| PubMed | Nucleotide | Protein | Genome | Structure | PMC | Taxonomy | OMIM | Books |

Search Protein ▾ for [   ] Go Clear

Display GenPept ▾ Show 20 ▾ Send to ▾

Range: from begin to end   Features: ☑ CDD [+] Refresh

☐ **1:** NP_288194. Reports glutamate dehydro...[gi:15802172]

BLink, Conserved
Domains, Links

Comment   Features   Sequence

```
LOCUS       NP_288194                447 aa            linear   BCT 18-JUL-2008
DEFINITION  glutamate dehydrogenase [Escherichia coli O157:H7 EDL933].
ACCESSION   NP_288194
VERSION     NP_288194.1  GI:15802172
DBSOURCE    REFSEQ: accession NC_002655.2
KEYWORDS    .
SOURCE      Escherichia coli O157:H7 EDL933
  ORGANISM  Escherichia coli O157:H7 EDL933
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1  (residues 1 to 447)
  AUTHORS   Perna,N.T., Plunkett,G. III, Burland,V., Mau,B., Glasner,J.D.,
            Rose,D.J., Mayhew,G.F., Evans,P.S., Gregor,J., Kirkpatrick,H.A.,
            Posfai,G., Hackett,J., Klink,S., Boutin,A., Shao,Y., Miller,L.,
            Grotbeck,E.J., Davis,N.W., Lim,A., Dimalanta,E., Potamousis,K.,
            Apodaca,J., Anantharaman,T.S., Lin,J., Yen,G., Schwartz,D.C.,
            Welch,R.A. and Blattner,F.R.
  TITLE     Genome sequence of enterohaemorrhagic Escherichia coli O157:H7
  JOURNAL   Nature 409 (6819), 529-533 (2001)
   PUBMED   11206551
REFERENCE   2  (residues 1 to 447)
  CONSRTM   NCBI Genome Project
  TITLE     Direct Submission
  JOURNAL   Submitted (28-SEP-2001) National Center for Biotechnology
            Information, NIH, Bethesda, MD 20894, USA
REFERENCE   3  (residues 1 to 447)
  AUTHORS   Perna,N.T., Plunkett,G. III, Burland,V., Mau,B., Glasner,J.D.,
            Rose,D.J., Mayhew,G.F., Evans,P.S., Gregor,J., Kirkpatrick,H.A.,
            Posfai,G., Hackett,J., Klink,S., Boutin,A., Shao,Y., Miller,L.,
            Grotbeck,E.J., Davis,N.W., Lim,A., Dimalanta,E., Potamousis,K.,
            Apodaca,J., Anantharaman,T.S., Lin,J., Yen,G., Schwartz,D.C.,
            Welch,R.A. and Blattner,F.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-2000) Laboratory of Genetics, University of
            Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
COMMENT     PROVISIONAL REFSEQ: This record has not yet been subject to final
            NCBI review. The reference sequence was derived from AAG56747.
            Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..447
                     /organism="Escherichia coli O157:H7 EDL933"
                     /strain="EDL933"
                     /serotype="O157:H7"
                     /db_xref="taxon:155864"
                     /note="enterohemorrhagic"
     Protein         1..447
                     /product="glutamate dehydrogenase"
                     /EC_number="1.4.1.4"
```

```
                        /function="enzyme; Amino acid biosynthesis: Glutamate"
                        /calculated_mol_wt=48438
        Region          6..447
                        /region_name="PRK09414"
                        /note="glutamate dehydrogenase; Provisional; PRK09414"
                        /db_xref="CDD:103887"
        Region          57..187
                        /region_name="ELFV_dehydrog_N"
                        /note="Glu/Leu/Phe/Val dehydrogenase, dimerisation domain;
                        pfam02812"
                        /db_xref="CDD:111682"
        Region          202..445
                        /region_name="NADB_Rossmann"
                        /note="Rossmann-fold NAD(P)(+)-binding proteins; cl09931"
                        /db_xref="CDD:127283"
        CDS             1..447
                        /gene="gdhA"
                        /locus_tag="Z2793"
                        /coded_by="NC_002655.2:2517086..2518429"
                        /note="converts 2-oxoglutarate to glutamate; in
                        Escherichia coli this enzyme plays a role in glutamate
                        synthesis when the cell is under energy restriction; uses
                        NADPH; forms a homohexamer"
                        /transl_table=11
                        /db_xref="GeneID:961732"
ORIGIN
        1 mdqtyslesf lnhvqkrdpn qtefaqavre vmttlwpfle qnpkyrqmsl lerlveperv
       61 iqfrvvwvdd rnqvqvnraw rvqfssaigp ykggmrfhps vnlsilkflg feqtfknalt
      121 tlpmgggkgg sdfdpkgkse gevmrfcqal mtelyrhlga dtdvpagdig vggrevgfma
      181 gmmkklsnnt acvftgkgls fggslirpea tgyglvyfte amlkrhgmgf egmrvsvsgs
      241 gnvaqyaiek amefgarvit asdssgtvvd esgftekla rlieikssrd grvadyakef
      301 glvylegqqp wsvpvdialp catqneldvd aahqliangv kavaeganmp ttieatelfq
      361 qagvlfapgk aanaggvats glemaqnaar lgwkaekvda rlhhimldih hacvehggeg
      421 eqtnyvqgan iagfvkvada mlaqgvi
//
```
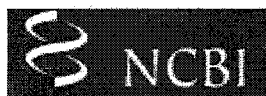
Search [Protein ▾] for [   ] [Go] [Clear]

Display [GenPept ▾] Show [20 ▾] [Send to ▾]

Range: from [begin   ] to [end   ]   Features: ☑ CDD [+]   [Refresh]

□ **1**: <u>NP_754056</u>. Reports glutamate dehydro...[gi:26248016]

BLink, Conserved
Domains, Links

<u>Comment</u>   <u>Features</u>   <u>Sequence</u>

```
LOCUS       NP_754056               447 aa            linear   BCT 20-JUL-2008
DEFINITION  glutamate dehydrogenase [Escherichia coli CFT073].
ACCESSION   NP_754056
VERSION     NP_754056.1  GI:26248016
DBSOURCE    REFSEQ: accession NC_004431.1
KEYWORDS    .
SOURCE      Escherichia coli CFT073
  ORGANISM  Escherichia coli CFT073
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1  (residues 1 to 447)
  AUTHORS   Welch,R.A., Burland,V., Plunkett,G.D. III, Redford,P., Roesch,P.,
            Rasko,D.A., Buckles,E.L., Liou,S.-R., Boutin,A., Hackett,J.,
            Stroud,D., Mayhew,G.F., Rose,D.J., Zhou,S., Schwartz,D.C.,
            Perna,N.T., Mobley,H.L.T., Donnenberg,M.S. and Blattner,F.R.
  TITLE     Extensive mosaic structure revealed by the complete genome sequence
            of uropathogenic Escherichia coli
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 17020-17024 (2002)
   PUBMED   12471157
REFERENCE   2  (residues 1 to 447)
  CONSRTM   NCBI Genome Project
  TITLE     Direct Submission
  JOURNAL   Submitted (10-SEP-2004) National Center for Biotechnology
            Information, NIH, Bethesda, MD 20894, USA
REFERENCE   3  (residues 1 to 447)
  AUTHORS   Welch,R.A., Burland,V., Plunkett,G.D. III, Redford,P., Roesch,P.,
            Rasko,D.A., Buckles,E.L., Liou,S.-R., Boutin,A., Hackett,J.,
            Stroud,D., Mayhew,G.F., Rose,D.J., Zhou,S., Schwartz,D.C.,
            Perna,N.T., Mobley,H.L.T., Donnenberg,M.S. and Blattner,F.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUN-2002) Genetics Laboratory, University of
            Wisconsin - Madison, 445 Henry Mall, Madison, WI 53706, USA
COMMENT     PROVISIONAL REFSEQ: This record has not yet been subject to final
            NCBI review. The reference sequence was derived from AAN80621.
            Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..447
                     /organism="Escherichia coli CFT073"
                     /strain="CFT073"
                     /db_xref="taxon:199310"
     Protein         1..447
                     /product="glutamate dehydrogenase"
                     /EC_number="1.4.1.4"
                     /function="enzyme; Amino acid biosynthesis: Glutamate"
                     /calculated_mol_wt=48438
     Region          6..447
                     /region_name="PRK09414"
                     /note="glutamate dehydrogenase; Provisional; PRK09414"
```

```
                           /db_xref="CDD:103887"
          Region           57..187
                           /region_name="ELFV_dehydrog_N"
                           /note="Glu/Leu/Phe/Val dehydrogenase, dimerisation domain;
                           pfam02812"
                           /db_xref="CDD:111682"
          Region           202..445
                           /region_name="NADB_Rossmann"
                           /note="Rossmann-fold NAD(P)(+)-binding proteins; cl09931"
                           /db_xref="CDD:127283"
          CDS              1..447
                           /gene="gdhA"
                           /locus_tag="c2162"
                           /coded_by="NC_004431.1:1996215..1997558"
                           /note="converts 2-oxoglutarate to glutamate; in
                           Escherichia coli this enzyme plays a role in glutamate
                           synthesis when the cell is under energy restriction; uses
                           NADPH; forms a homohexamer"
                           /transl_table=11
                           /db_xref="GeneID:1036597"
ORIGIN
        1 mdqtyslesf lnhvqkrdpn qtefaqavre vmttlwpfle qnpkyrqmsl lerlveperv
       61 iqfrvvwvdd rnqvqvnraw rvqfssaigp ykggmrfhps vnlsilkflg feqtfknalt
      121 tlpmgggkgg sdfdpkgkse gevmrfcqal mtelyrhlga dtdvpagdig vggrevgfma
      181 gmmkklsnnt acvftgkgls fggslirpea tgyglvyfte amlkrhgmgf egmrvsvsgs
      241 gnvaqyaiek amefgarvit asdssgtvvd esgftkekla rlieikasrd grvadyakef
      301 glvylegqqp wsvpvdialp catqneldvd aahqliangv kavaeganmp ttieatelfq
      361 qagvlfapgk aanaggvats glemaqnaar lgwkaekvda rlhhimldih hacvehggeg
      421 eqtnyvqgan iagfvkvada mlsqgvi
//
```
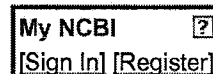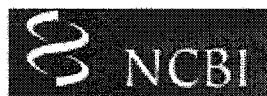
NCBI

●●●●● ●● ● ● ●●●●●● ●● ●●●●●●● *Entrez* Protein

My NCBI   [?]
[Sign In] [Register]

Search Protein ▾ for [   ] [Go] [Clear]

Display GenPept ▾ Show 20 ▾ Send to ▾

Range: from begin [   ] to end [   ]   Features: ☑ CDD [+]   [Refresh]

☐ **1:** ZP_03049943. Reports NADP-specific glu...[gi:193068984]

BLink, Conserved
Domains, Links

Comment   Features   Sequence

```
LOCUS       ZP_03049943            447 aa            linear   BCT 25-JUN-2008
DEFINITION  NADP-specific glutamate dehydrogenase [Escherichia coli E110019].
ACCESSION   ZP_03049943
VERSION     ZP_03049943.1  GI:193068984
DBSOURCE    REFSEQ: accession NZ_AAJW02000011.1
KEYWORDS    .
SOURCE      Escherichia coli E110019
  ORGANISM  Escherichia coli E110019
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1  (residues 1 to 447)
  AUTHORS   Rasko,D., Rosovitz,M., Myers,G., Seshadri,R., Cer,R., Jiang,L.,
            Ravel,J., Fricke,W.F. and Sebastian,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUN-2008) J. Craig Venter Institute, 9704 Medical
            Center Drive, Rockville, MD 20850, USA
REFERENCE   2  (residues 1 to 447)
  AUTHORS   Rasko,D.A., Rosovitz,M.J., Kaper,J.B., Myers,G.S.A., Seshadri,R.,
            Cer,R.Z., Jiang,L. and Ravel,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-2005) The Institute for Genomic Research, 9712
            Medical Center Drive, Rockville, MD 20850, USA
COMMENT     PREDICTED REFSEQ: This record has not been reviewed and the
            function is unknown. The reference sequence was derived from
            EDV88223.
            Escherichia coli E110019 was isolated from an outbreak in Finland
            (Viljanen MK et al, Lancet (1990), 336(8719): 831-4).  The outbreak
            affected approximately 650 students at a school. In a fashion
            uncommon in other EPEC strains, E. coli E110019 spread from
            person-to-person to over 100 close contacts outside of the school
            setting. E. coli E110019 represents an atypical enteropathogenic E.
            coli (atypical EPEC) characterized by the lack of previously
            identified EPEC virulence factors including the EAF plasmid.
            E110019 is serotype O111:H9.
            Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..447
                     /organism="Escherichia coli E110019"
                     /strain="E110019"
                     /serovar="O111:H9"
                     /db_xref="taxon:340186"
     Protein         1..447
                     /product="NADP-specific glutamate dehydrogenase"
                     /calculated_mol_wt=48452
     Region          6..447
                     /region_name="PRK09414"
                     /note="glutamate dehydrogenase; Provisional; PRK09414"
                     /db_xref="CDD:103887"
```

```
        Region             57..187
                           /region_name="ELFV_dehydrog_N"
                           /note="Glu/Leu/Phe/Val dehydrogenase, dimerisation domain;
                           pfam02812"
                           /db_xref="CDD:111682"
        Region             202..445
                           /region_name="NADB_Rossmann"
                           /note="Rossmann-fold NAD(P)(+)-binding proteins; cl09931"
                           /db_xref="CDD:127283"
        CDS                1..447
                           /gene="gdhA"
                           /locus_tag="EcE110019_3311"
                           /coded_by="complement(NZ_AAJW02000011.1:36581..37924)"
                           /note="identified by match to protein family HMM PF00208;
                           match to protein family HMM PF02812"
                           /transl_table=11
ORIGIN
        1 mdqtyslesf lnhvqkrdpn qtefaqavre vmttlwpfle qnpkyrqmsl lerlveperv
       61 iqfrvvwvdd rnqvqvnraw rvqfssaigp ykggmrfhps vnlsilkflg feqtfknalt
      121 tlpmgggkgg sdfdpkgkse gevmrfcqal mtelyrhlga dtdvpagdig vggrevgfma
      181 gmmkklsnnt acvftgkgls fggslirpea tgyglvyfte amlkrhgmgf egmrvsvsgs
      241 gnvaqyaiek amefgarvit asdssgtvvd esgftkekla rlieikasrd grvadyakef
      301 glvylegqqp wsvpvdialp catqneldvd aahqliangv kavaeganmp ttieatelfq
      361 qagvlfapgk aanaggvats glemaqnaar lgwkaekvda rlhhimldih hacvehggeg
      421 eqtnyvqgan iasfvkvada mlaqgvi
//
```
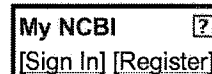
NCBI ●●●●● ●● ●●●● ●●●● ●●● ●●●●● ●●●●● Entrez Protein

| PubMed | Nucleotide | Protein | Genome | Structure | PMC | Taxonomy | OMIM | Books |

Search Protein for [   ] Go Clear

Display GenPept Show 20 Send to

Range: from begin to end   Features: ☑ CDD + Refresh

☐ **1:** YP_001463059. Reports glutamate dehydro...[gi:157158996]

BLink, Conserved
Domains, Links

Comment   Features   Sequence

```
LOCUS       YP_001463059            447 aa            linear   BCT 25-JUL-2008
DEFINITION  glutamate dehydrogenase [Escherichia coli E24377A].
ACCESSION   YP_001463059
VERSION     YP_001463059.1  GI:157158996
DBSOURCE    REFSEQ: accession NC_009801.1
KEYWORDS    .
SOURCE      Escherichia coli E24377A
  ORGANISM  Escherichia coli E24377A
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1  (residues 1 to 447)
  CONSRTM   NCBI Genome Project
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2007) National Center for Biotechnology
            Information, NIH, Bethesda, MD 20894, USA
REFERENCE   2  (residues 1 to 447)
  AUTHORS   Rasko,D.A., Rosovitz,M.J., Brinkley,C., Myers,G.S.A., Seshadri,R.,
            Cer,R.Z., Jiang,L. and Ravel,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-AUG-2007) The Institute for Genomic Research, 9712
            Medical Center Dr., Rockville, MD 20850, USA
COMMENT     PROVISIONAL REFSEQ: This record has not yet been subject to final
            NCBI review. The reference sequence was derived from ABV20734.
            Source DNA and bacteria available from Jacques Ravel
            (jravel@tigr.org).
            Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..447
                     /organism="Escherichia coli E24377A"
                     /strain="E24377A"
                     /db_xref="taxon:331111"
     Protein         1..447
                     /product="glutamate dehydrogenase"
                     /calculated_mol_wt=48422
     Region          6..447
                     /region_name="PRK09414"
                     /note="glutamate dehydrogenase; Provisional; PRK09414"
                     /db_xref="CDD:103887"
     Region          57..187
                     /region_name="ELFV_dehydrog_N"
                     /note="Glu/Leu/Phe/Val dehydrogenase, dimerisation domain;
                     pfam02812"
                     /db_xref="CDD:111682"
     Region          202..445
                     /region_name="NADB_Rossmann"
                     /note="Rossmann-fold NAD(P)(+)-binding proteins; cl09931"
                     /db_xref="CDD:127283"
     CDS             1..447
```

```
                    /gene="gdhA"
                    /locus_tag="EcE24377A_1984"
                    /coded_by="NC_009801.1:1967993..1969336"
                    /note="converts 2-oxoglutarate to glutamate; in
                    Escherichia coli this enzyme plays a role in glutamate
                    synthesis when the cell is under energy restriction; uses
                    NADPH; forms a homohexamer"
                    /transl_table=11
                    /db_xref="GeneID:5589791"
ORIGIN
        1 mdqtyslesf lnhvqkrdpn qtefaqavre vmttlwpfle qnpkyrqmsl lerlveperv
       61 iqfrvvwvdd rnqvqvnraw rvqfssaigp ykggmrfhps vnlsilkflg feqtfknalt
      121 tlpmgggkgg sdfdpkgkse gevmrfcqal mtelyrhlga dtdvpagdig vggrevgfma
      181 gmmkklsnnt acvftgkgls fggslirpea tgyglvyfte amlkrhgmgf egmrvsvsgs
      241 gnvaqyaiek amefgarvit asdssgtvvd esgftkekla rlieikasrd grvadyakef
      301 glvylegqqp wsvpvdialp catqneldvd aahqliangv kavaeganmp ttieatelfq
      361 qagvlfapgk aanaggvats glemaqnaar lgwkaekvda rlhhimldih hacvehggeg
      421 eqtnyvqgan iagfvkvada mlaqgvi
//
```

Last update: Mon, 12 Jan 2009 Rev. 149544

Search [Protein ▼] for [_____] [Go] [Clear]

Display [GenPept ▼] Show [20 ▼] [Send to ▼]

Range: from [begin____] to [end____]   Features: ☑ CDD [+] [Refresh]

☐ **1:** YP_002407302. Reports glutamate dehydro...[gi:218699673]

BLink, Conserved
Domains, Links

Comment   Features   Sequence

```
LOCUS       YP_002407302              447 aa                linear   BCT 22-DEC-2008
DEFINITION  glutamate dehydrogenase, NADP-specific [Escherichia coli IAI39].
ACCESSION   YP_002407302
VERSION     YP_002407302.1  GI:218699673
DBSOURCE    REFSEQ: accession NC_011750.1
KEYWORDS    .
SOURCE      Escherichia coli IAI39
  ORGANISM  Escherichia coli IAI39
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1  (residues 1 to 447)
  CONSRTM   NCBI Genome Project
  TITLE     Direct Submission
  JOURNAL   Submitted (18-DEC-2008) National Center for Biotechnology
            Information, NIH, Bethesda, MD 20894, USA
REFERENCE   2  (residues 1 to 447)
  AUTHORS   Genoscope -,C.E.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-DEC-2008) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     PROVISIONAL REFSEQ: This record has not yet been subject to final
            NCBI review. The reference sequence was derived from CAR17428.
            Annotation results relative to BLAST similarities, COG
            assignations, enzymatic function prediction (PRIAM software), TMHMM
            and SignalP predictions, and synteny conservation (Syntonizer
            software) are available in the MaGe annotation system
            http://www.genoscope.cns.fr/agc/mage.
            Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..447
                     /organism="Escherichia coli IAI39"
                     /strain="IAI39"
                     /db_xref="taxon:585057"
     Protein         1..447
                     /product="glutamate dehydrogenase, NADP-specific"
                     /EC_number="1.4.1.4"
                     /function="1.3 : Glutamate family"
                     /calculated_mol_wt=48424
     Region          6..447
                     /region_name="PRK09414"
                     /note="glutamate dehydrogenase; Provisional; PRK09414"
                     /db_xref="CDD:103887"
     Region          57..187
                     /region_name="ELFV_dehydrog_N"
                     /note="Glu/Leu/Phe/Val dehydrogenase, dimerisation domain;
                     pfam02812"
                     /db_xref="CDD:111682"
```

```
     Region                202..445
                           /region_name="NADB_Rossmann"
                           /note="Rossmann-fold NAD(P)(+)-binding proteins; cl09931"
                           /db_xref="CDD:127283"
     CDS                   1..447
                           /gene="gdhA"
                           /locus_tag="ECIAI39_1294"
                           /coded_by="complement(NC_011750.1:1359809..1361152)"
                           /inference="ab initio prediction:AMIGene:2.0"
                           /note="Evidence 1b : Function experimentally demonstrated
                           in the studied species; PubMedId : 75128035, 76046227,
                           94321339, 6308576, 6373501, 9298646; Product type e :
                           enzyme"
                           /transl_table=11
                           /db_xref="GeneID:7153003"
ORIGIN
        1 mdqtyslesf lnhvqkrdpn qtefaqavre vmttlwpfle qnpkyrqmsl lerlveperv
       61 iqfrvvwvdd rnqvqvnraw rvqfssaigp ykggmrfhps vnlsilkflg feqtfknalt
      121 tlpmgggkgg sdfdpkgkse gevmrfcqal mtelyrhlga dtdvpagdig vggrevgfma
      181 gmmkklsnnt acvftgkgls fggslirpea tgyglvyfte amlkrhgmgf egmrvsvsgs
      241 gnvaqyaiek amefgarvit asdssgtvvd esgftkekla rlieikasrd grvadyakef
      301 glvylegqqp wsvpvdialp catqneldvd aahqliangv kavaeganmp ttieatelfq
      361 qagvlfapgk aanaggvats glemaqnaar lgwkaekvda rlhhimldih hacvehggeg
      421 dqtnyvqgan iagfvkvada mlsqgvi
//
```

Last update: Mon, 12 Jan 2009 Rev. 149544